SEQUENCE LISTING

<110> Brice, Alexis
Koutnikova, Hana
Fournier, Alain
Pradier, Laurent
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Arnould-Reguigne, Isabelle
Rosier-Montus, Marie-Francoise
Corti, Olga

<120> COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF PARKIN

<130> ST00005

<140> 09/785,548
<141> 2001-02-20

<160> 50

<170> PatentIn Version 3.2

<210> 1
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<213> Homo sapiens

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Gln Asn Leu Pro Ser Ser Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly
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ttt aga cac gga agt tta att agc att gac agc acc tgt aca gag atg   96
Phe Arg His Gly Ser Leu Ile Ser Ile Asp Ser Thr Cys Thr Glu Met
             20                  25                  30

ggc aat ttt gac aat gct aat gtc act gga gaa ata gaa ttt gcc att   144
Gly Asn Phe Asp Asn Ala Asn Val Thr Gly Glu Ile Glu Phe Ala Ile
         35                  40                  45

cat tat tgc ttc aaa acc cat tct tta gaa ata tgc atc aag gcc tgt   192
His Tyr Cys Phe Lys Thr His Ser Leu Glu Ile Cys Ile Lys Ala Cys
     50                  55                  60

aag aac ctt gcc tat gga gaa gaa aag aag aaa aag tgc aat ccg tat   240
Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr
 65                  70                  75                  80

gtg aag acc tac ctg ttg ccc gac aga tcc tcc cag gga aag cgc aag   288
Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys
                 85                  90                  95

act gga gtc caa agg aac acc gtg gac ccg acc ttt cag gag acc ttg   336
Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr Leu
            100                 105                 110

aag tat cag gtg gcc cct gcc cag ctg gtg acc cgg cag ctg cag gtc   384
Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln Val
        115                 120                 125

tcg gtg tgg cat ctg ggc acg ctg gcc cgg aga gtg ttt ctt gga gaa   432
Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly Glu
    130                 135                 140
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Val Ile Ile Ser Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln
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tcc ttc cgc tgg cat ccg ctc cgg gcc aag gcg gag aaa tac gaa gac   528
Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp
                165                 170                 175

agc gtt cct cag agt aat gga gag ctc aca gtc cgg gct aag ctg gtt   576
Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu Val
            180                 185                 190

ctc cct tca cgg ccc aga aaa ctc caa gag gct caa gaa ggg aca gat   624
Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp
        195                 200                 205

cag cca tca ctt cat ggt caa ctt tgt ttg gta gtg cta gga gcc aag   672
Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala Lys
    210                 215                 220

aat tta cct gtg cgg cca gat ggc acc ttg aac tca ttt gtt aag ggc   720
Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys Gly
225                 230                 235                 240

tgt ctc act ctg cca gac caa caa aaa ctg aga ctg aag tcg cca gtc   768
Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro Val
                245                 250                 255

ctg agg aag cag gct tgc ccc cag tgg aaa cac tca ttt gtc ttc agt   816
Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe Ser
            260                 265                 270

ggc gta acc cca gct cag ctg agg cag tcg agc ttg gag tta act gtc   864
Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr Val
        275                 280                 285

tgg gat cag gcc ctc ttt gga atg aat gac cgc ttg ctt gga gga acc   912
Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly Thr
    290                 295                 300

aga ctt ggt tca aag gga gac aca gct gtt ggc ggg gat gca tgc tca   960
Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys Ser
305                 310                 315                 320

cta tcg aag ctc cag tgg cag aaa gtc ctt tcc agc ccc aat cta tgg   1008
Leu Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu Trp
                325                 330                 335

aca gac atg act ctt gtc ctg cac tgacatgaag gcctcaaggt tccaggttgc  1062
Thr Asp Met Thr Leu Val Leu His
            340

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<213> Homo sapiens

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20 25 30

Gly Asn Phe Asp Asn Ala Asn Val Thr Gly Glu Ile Glu Phe Ala Ile
35 40 45

His Tyr Cys Phe Lys Thr His Ser Leu Glu Ile Cys Ile Lys Ala Cys
50 55 60

Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr
65 70 75 80

Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys
85 90 95

Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr Leu
100 105 110

Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln Val
115 120 125

Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly Glu
130 135 140

Val Ile Ile Ser Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln
145 150 155 160

Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp
165 170 175

Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu Val
180 185 190

Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp
195 200 205

Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala Lys
210 215 220

Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys Gly
225 230 235 240

Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro Val
245 250 255

Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe Ser
260 265 270

Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr Val
275 280 285

Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly Thr
290 295 300

Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys Ser
305 310 315 320

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Leu Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu Trp
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Thr Asp Met Thr Leu Val Leu His
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<213> Homo sapiens

<220>
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Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn Ser Phe Tyr Val Tyr Cys
  1               5                  10                  15

aaa ggc ccc tgt caa aga gtg cag ccg gga aaa ctc agg gta cag tgc   96
Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln Cys
             20                  25                  30

agc acc tgc agg cag gca acg ctc acc ttg acc cag ggt cca tct tgc   144
Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu Thr Gln Gly Pro Ser Cys
         35                  40                  45

tgg gat gat gtt tta att cca aac cgg atg agt ggt gaa tgc caa tcc   192
Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser
     50                  55                  60

cca cac tgc cct ggg act agt gca gaa ttt ttc ttt aaa tgt gga gca   240
Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly Ala
 65                  70                  75                  80

cac ccc acc tct gac aag gaa aca tca gta gct ttg cac ctg atc gca   288
His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile Ala
                85                  90                  95

aca aat agt cgg aac atc act tgc att acg tgc aca gac gtc agg agc   336
Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg Ser
            100                 105                 110

ccc gtc ctg gtt ttc cag tgc aac tcc cgc cac gtg att tgc tta gac   384
Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu Asp
        115                 120                 125

tgt ttc cac tta tac tgt gtg aca aga ctc aat gat cgg cag ttt gtt   432
Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val
    130                 135                 140

cac gac cct caa ctt ggc tac tcc ctg cct tgt gtg tag               471
His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val
145                 150                 155
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<210> 4
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<212> PRT
<213> Homo sapiens

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20 25 30
Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu Thr Gln Gly Pro Ser Cys
35 40 45
Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser
50 55 60
Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly Ala
65 70 75 80
His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile Ala
85 90 95
Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg Ser
100 105 110
Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu Asp
115 120 125
Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val
130 135 140
His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val
145 150 155

<210> 5
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<213> Artificial sequence

<220>
<223> Description of the artificial sequence:Oligonucleotide

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<210> 6
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<212> DNA
<213> Artificial sequence

<220>
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<210> 7
<211> 19
<212> DNA
<213> Artificial sequence

<220>
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<400> 7
gcgtttggaa tcactacag 19

<210> 8
<211> 17
<212> DNA

<213> Artificial sequence

<220>
<223> Description of the artificial sequence:Oligonucleotide

<400> 8
ggtctcggtg tggcatc 17

<210> 9
<211> 18
<212> DNA
<213> Artificial sequence

<220>
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<400> 9
ccgcttgctt ggaggaac 18

<210> 10
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:Oligonucleotide

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<210> 11
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:Oligonucleotide

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<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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             20                  25                  30

Glu Glu Arg Thr Arg Lys Leu Lys Thr His Leu Gln His Leu Arg Trp
         35                  40                  45

Lys Gly Ala Lys Asn Thr Asp Trp Glu His Lys Glu Lys Cys Cys Ala
     50                  55                  60

Arg Cys Gln Gln Val Leu Gly Phe Leu Leu His Arg Gly Ala Val Cys
 65                  70                  75                  80

Arg Gly Cys Ser His Arg Val Cys Ala Gln Cys Arg Val Phe Leu Arg
                85                  90                  95

Gly Thr His Ala Trp Lys Cys Thr Val Cys Phe Glu Asp Arg Asn Val
            100                 105                 110

Lys Ile Lys Thr Gly Glu Trp Phe Tyr Glu Glu Arg Ala Lys Lys Phe
        115                 120                 125

Pro Thr Gly Gly Lys His Glu Thr Val Gly Gly Gln Leu Leu Gln Ser
    130                 135                 140

Tyr Gln Lys Leu Ser Lys Ile Ser Val Val Pro Pro Thr Pro Pro Pro
145                 150                 155                 160
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Val Ser Glu Ser Gln Cys Ser Arg Ser Pro Gly Arg Leu Gln Glu Phe
165 170 175

Gly Gln Phe Arg Gly Phe Asn Lys Ser Val Glu Asn Leu Phe Leu Ser
180 185 190

Leu Ala Thr His Val Lys Lys Leu Ser Lys Ser Gln Asn Asp Met Thr
195 200 205

Ser Glu Lys His Leu Leu Ala Thr Gly Pro Arg Gln Cys Val Gly Gln
210 215 220

Thr Glu Arg Arg Ser Gln Ser Asp Thr Ala Val Asn Val Thr Thr Arg
225 230 235 240

Lys Val Ser Ala Pro Asp Ile Leu Lys Pro Leu Asn Gln Glu Asp Pro
245 250 255

Lys Cys Ser Thr Asn Pro Ile Leu Lys Gln Gln Asn Leu Pro Ser Ser
260 265 270

Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly Phe Arg His Gly Ser Leu
275 280 285

Ile Ser Ile Asp Ser Thr Cys Thr Glu Met Gly Asn Phe Asp Asn Ala
290 295 300

Asn Val Thr Gly Glu Ile Glu Phe Ala Ile His Tyr Cys Phe Lys Thr
305 310 315 320

His Ser Leu Glu Ile Cys Ile Lys Ala Cys Lys Asn Leu Ala Tyr Gly
325 330 335

Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr Val Lys Thr Tyr Leu Leu
340 345 350

Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys Thr Gly Val Gln Arg Asn
355 360 365

Thr Val Asp Pro Thr Phe Gln Glu Thr Leu Lys Tyr Gln Val Ala Pro
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Ala Gln Leu Val Thr Arg Gln Leu Gln Val Ser Val Trp His Leu Gly
385 390 395 400

Thr Leu Ala Arg Arg Val Phe Leu Gly Glu Val Ile Ile Pro Leu Ala
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Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln Ser Phe Arg Trp His Pro
420 425 430

Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp Ser Val Pro Gln Ser Asn
435 440 445

Gly Glu Leu Thr Val Arg Ala Lys Leu Val Leu Pro Ser Arg Pro Arg
450 455 460

Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp Gln Pro Ser Leu His Gly
465 470 475 480

Gln Leu Cys Leu Val Val Leu Gly Ala Lys Asn Leu Pro Val Arg Pro
485 490 495

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Asp Gly Thr Leu Asn Ser Phe Val Lys Gly Cys Leu Thr Leu Pro Asp
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Gln Gln Lys Leu Arg Leu Lys Ser Pro Val Leu Arg Lys Gln Ala Cys
        515                 520                 525

Pro Gln Trp Lys His Ser Phe Val Phe Ser Gly Val Thr Pro Ala Gln
    530                 535                 540

Leu Arg Gln Ser Ser Leu Glu Leu Thr Val Trp Asp Gln Ala Leu Phe
545                 550                 555                 560

Gly Met Asn Asp Arg Leu Leu Gly Gly Thr Arg Leu Gly Ser Lys Gly
                565                 570                 575

Asp Thr Ala Val Gly Gly Asp Ala Cys Ser Gln Ser Lys Leu Gln Trp
            580                 585                 590

Gln Lys Val Leu Ser Ser Pro Asn Leu Trp Thr Asp Met Thr Leu Val
        595                 600                 605

Leu His
    610
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<213> Homo sapiens

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<210> 15
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<212> PRT

<213> Homo sapiens

<400> 15

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            20                  25                  30

Cys Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Lys Cys Asn Pro
         35                  40                  45

Tyr Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg
     50                  55                  60

Lys Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr
 65                  70                  75                  80

Leu Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln
                85                  90                  95

Val Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly
            100                 105                 110

Glu Val Ile Ile Pro Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr
        115                 120                 125

Gln Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu
    130                 135                 140

Asp Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu
145                 150                 155                 160

Val Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr
                165                 170                 175

Asp Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala
            180                 185                 190

Lys Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys
        195                 200                 205

Gly Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro
    210                 215                 220

Val Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe
225                 230                 235                 240

Ser Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr
                245                 250                 255

Val Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly
            260                 265                 270

Thr Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys
        275                 280                 285

Ser Gln Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu
    290                 295                 300

Trp Thr Asp Met Thr Leu Val Leu His
305                 310
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<210> 16
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 16
ccagttctgc ctgttcatc 19

<210> 17
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 17
ttcaaaacac agaggaggag 20

<210> 18
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 18
gaatttggtc agtttagagg 20

<210> 19
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 19
ttctgggatt tggagagctt tttcac 26

<210> 20
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 20
tctgtctgtc ccacacactg cc 22

<210> 21
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 21
gactggctcc gtctctctg 19

<210> 22
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 22
aagcaacaga atctcccatc c 21

<210> 23
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 23
gcattgtcaa aattgcccat c 21

<210> 24
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 24
aggcggagaa atacgaagac 20

<210> 25
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 25
gcagagtgag acagccctta ac 22

<210> 26
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 26
cttcctcagg actggcgact tcag 24

<210> 27
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 27
caagcggtcg ttcattccaa agag 24

<210> 28
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 28
aagaggagat aacccaccag ag 22

<210> 29
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 29
agggctgctg gctatttttc 20

<210> 30
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 30
taagaaatgg gttgtgaac 19

<210> 31
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 31
aagcaacaga atctcccatc c 21

<210> 32
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 32
gcattgtcaa aattgcccat c 21

<210> 33
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 33
aggcggagaa atacgaagac 20

<210> 34
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 34
gcagagtgag acagccctta ac 22

<210> 35
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 35
cttcctcagg actggcgact tcag 24

<210> 36
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 36
caagcggtcg ttcattccaa agag 24

<210> 37
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 37
aagaggagat aacccaccag ag 22

<210> 38
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 38
aatggaaggg cgtgacgc 18

<210> 39
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 39
cctcacgcct gctgcaacct g 21

<210> 40
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 40
gcacgaattc atggcccaag aaatagatct g 31

<210> 41
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 41
ctgtcttcgt atttctccgc cttg 24

<210> 42
<211> 2347
<212> DNA
<213> Homo sapiens

<220>
<223> Delete: this sequence is a duplicate of Sequence 12

<400> 42
ggccttgggg cactgaggga tgccagttct gcctgttcat ctggaacctg gatctaagga 60
gggaagaggc gttgcccctg ctggcatagt caggtaccag cccagccagg tattgaacgg 120
gctgagcttt tcatgatggt tcctgctgac ctggaaacat cttaaatgga agggcgtgag 180
cgcttggtcc atgcagtgaa gctcttccaa cctgggtcaa cgaaaacgga gaagaaatgg 240
cccaagaaat agatctgagt gctctcaagg agttagaacg cgaggccatt ctccaggtcc 300
tgtaccgaga ccaggcggtt caaaacacag aggaggagag gacacggaaa ctgaaaacac 360
acctgcagca tctccggtgg aaaggagcga agaacacgga ctgggagcac aaagagaagt 420
gctgtgcgcg ctgccagcag gtgctggggt tcctgctgca ccggggcgcc gtgtgccggg 480
gctgcagcca ccgcgtgtgt gcccagtgcc gagtgttcct gaggggggacc catgcctgga 540
agtgcacggt gtgcttcgag gacaggaatg tcaaaataaa aactggagaa tggttctatg 600
aggaacgagc caagaaattt ccaactggag gcaaacatga gacagttgga gggcagctct 660
tgcaatctta tcagaagctg agcaaaattt ctgtggttcc tcctactcca cctcctgtca 720
gcgagagcca gtgcagccgc agtcctggca ggttacagga atttggtcag tttagaggat 780
ttaataagtc cgtggaaaat ttgtttctgt ctcttgctac ccacgtgaaa aagctctcca 840
aatcccagaa tgatatgact tctgagaagc atcttctcgc cacgggcccc aggcagtgtg 900
tgggacagac agagagacgg agccagtctg acactgcggt caacgtcacc accaggaagg 960
tcagtgcacc agatattctg aaacctctca atcaagagga tcccaaatgc tctactaacc 1020
ctattttgaa gcaacagaat ctcccatcca gtccggcacc cagtaccata ttctctggag 1080
gttttagaca cggaagttta attagcattg acagcacctg tacagagatg ggcaattttg 1140
acaatgctaa tgtcactgga gaaatagaat ttgccattca ttattgcttc aaaacccatt 1200
ctttagaaat atgcatcaag gcctgtaaga accttgccta tggagaagaa aagaagaaaa 1260
agtgcaatcc gtatgtgaag acctacctgt tgcccgacag atcctcccag ggaaagcgca 1320
agactggagt ccaaaggaac accgtggacc cgacctttca ggagaccttg aagtatcagg 1380
tggcccctgc ccagctggtg acccggcagc tgcaggtctc ggtgtggcat ctgggcacgc 1440
tggcccggag agtgtttctt ggagaagtga tcattcctct ggccacgtgg gactttgaag 1500
acagcacaac acagtccttc cgctggcatc cgctccgggc caaggcggag aaatacgaag 1560
acagcgttcc tcagagtaat ggagagctca cagtccgggc taagctggtt ctcccttcac 1620
ggcccagaaa actccaagag gctcaagaag ggacagatca gccatcactt catggtcaac 1680
tttgtttggt agtgctagga gccaagaatt tacctgtgcg gccagatggc accttgaact 1740
catttgttaa gggctgtctc actctgccag accaacaaaa actgagactg aagtcgccag 1800
tcctgaggaa gcaggcttgc ccccagtgga aacactcatt tgtcttcagt ggcgtaaccc 1860
cagctcagct gaggcagtcg agcttggagt taactgtctg ggatcaggcc ctctttggaa 1920
tgaacgaccg cttgcttgga ggaaccagac ttggttcaaa gggagacaca gctgttggcg 1980
gggatgcatg ctcacaatcg aagctccagt ggcagaaagt cctttccagc cccaatctat 2040
ggacagacat gactcttgtc ctgcactgac atgaaggcct caaggttcca ggttgcagca 2100
ggcgtgaggc actgtgcgtc tgcagagggg ctacgaacca ggtgcagggt cccagctgga 2160
gacccctttg accttgagca gtctccatct gcggccctgt cccatggctt aaccgcctat 2220
tggtatctgt gtatatttac gttaaacaca attatgttac ctaagcctct ggtgggttat 2280
ctcctctttg agatgtagaa aatggccaga ttttaataaa cgttgttacc catgaaaaaa 2340
aaaaaaa 2347

<210> 43
<211> 610
<212> PRT
<213> Homo sapiens

<220>
<223> Delete: this sequence is a duplicate of Sequence 13

<400> 43
Met Ala Gln Glu Ile Asp Leu Ser Ala Leu Lys Glu Leu Glu Arg Glu
1 5 10 15

Ala Ile Leu Gln Val Leu Tyr Arg Asp Gln Ala Val Gln Asn Thr Glu
20 25 30

Glu Glu Arg Thr Arg Lys Leu Lys Thr His Leu Gln His Leu Arg Trp
35 40 45

Lys Gly Ala Lys Asn Thr Asp Trp Glu His Lys Glu Lys Cys Cys Ala
50 55 60

```
Arg Cys Gln Gln Val Leu Gly Phe Leu Leu His Arg Gly Ala Val Cys
 65                  70                  75                  80

Arg Gly Cys Ser His Arg Val Cys Ala Gln Cys Arg Val Phe Leu Arg
                 85                  90                  95

Gly Thr His Ala Trp Lys Cys Thr Val Cys Phe Glu Asp Arg Asn Val
            100                 105                 110

Lys Ile Lys Thr Gly Glu Trp Phe Tyr Glu Glu Arg Ala Lys Lys Phe
        115                 120                 125

Pro Thr Gly Gly Lys His Glu Thr Val Gly Gly Gln Leu Leu Gln Ser
    130                 135                 140

Tyr Gln Lys Leu Ser Lys Ile Ser Val Val Pro Pro Thr Pro Pro Pro
145                 150                 155                 160

Val Ser Glu Ser Gln Cys Ser Arg Ser Pro Gly Arg Leu Gln Glu Phe
                165                 170                 175

Gly Gln Phe Arg Gly Phe Asn Lys Ser Val Glu Asn Leu Phe Leu Ser
            180                 185                 190

Leu Ala Thr His Val Lys Lys Leu Ser Lys Ser Gln Asn Asp Met Thr
        195                 200                 205

Ser Glu Lys His Leu Leu Ala Thr Gly Pro Arg Gln Cys Val Gly Gln
    210                 215                 220

Thr Glu Arg Arg Ser Gln Ser Asp Thr Ala Val Asn Val Thr Thr Arg
225                 230                 235                 240

Lys Val Ser Ala Pro Asp Ile Leu Lys Pro Leu Asn Gln Glu Asp Pro
                245                 250                 255

Lys Cys Ser Thr Asn Pro Ile Leu Lys Gln Gln Asn Leu Pro Ser Ser
            260                 265                 270

Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly Phe Arg His Gly Ser Leu
        275                 280                 285

Ile Ser Ile Asp Ser Thr Cys Thr Glu Met Gly Asn Phe Asp Asn Ala
    290                 295                 300

Asn Val Thr Gly Glu Ile Glu Phe Ala Ile His Tyr Cys Phe Lys Thr
305                 310                 315                 320

His Ser Leu Glu Ile Cys Ile Lys Ala Cys Lys Asn Leu Ala Tyr Gly
                325                 330                 335

Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr Val Lys Thr Tyr Leu Leu
            340                 345                 350

Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys Thr Gly Val Gln Arg Asn
        355                 360                 365

Thr Val Asp Pro Thr Phe Gln Glu Thr Leu Lys Tyr Gln Val Ala Pro
    370                 375                 380

Ala Gln Leu Val Thr Arg Gln Leu Gln Val Ser Val Trp His Leu Gly
385                 390                 395                 400

Thr Leu Ala Arg Arg Val Phe Leu Gly Glu Val Ile Ile Pro Leu Ala
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405 410 415

Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln Ser Phe Arg Trp His Pro
420 425 430

Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp Ser Val Pro Gln Ser Asn
435 440 445

Gly Glu Leu Thr Val Arg Ala Lys Leu Val Leu Pro Ser Arg Pro Arg
450 455 460

Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp Gln Pro Ser Leu His Gly
465 470 475 480

Gln Leu Cys Leu Val Val Leu Gly Ala Lys Asn Leu Pro Val Arg Pro
485 490 495

Asp Gly Thr Leu Asn Ser Phe Val Lys Gly Cys Leu Thr Leu Pro Asp
500 505 510

Gln Gln Lys Leu Arg Leu Lys Ser Pro Val Leu Arg Lys Gln Ala Cys
515 520 525

Pro Gln Trp Lys His Ser Phe Val Phe Ser Gly Val Thr Pro Ala Gln
530 535 540

Leu Arg Gln Ser Ser Leu Glu Leu Thr Val Trp Asp Gln Ala Leu Phe
545 550 555 560

Gly Met Asn Asp Arg Leu Leu Gly Gly Thr Arg Leu Gly Ser Lys Gly
565 570 575

Asp Thr Ala Val Gly Gly Asp Ala Cys Ser Gln Ser Lys Leu Gln Trp
580 585 590

Gln Lys Val Leu Ser Ser Pro Asn Leu Trp Thr Asp Met Thr Leu Val
595 600 605

Leu His
610

<210> 44
<211> 1648
<212> DNA
<213> Homo sapiens

<220>
<223> Delete: this sequence is a duplicate of Sequence 14

<400> 44
gaaatcatgc ccctcgtaga gcagcaggtc caagcagggc tgctggctat ttttccaaaa 60
agtgaggcag tttaaaaaaa aggcggagaa ctagaattat agaataatgg cacattttgt 120
gtatttgtaa aactaacggc ttgcatggtt cacaacccat ttcttatgcc tgtgttttcc 180
ttggcagcaa aatttctgtg gttcctccta ctccacctcc tgtcagcgag agccagtgca 240
gccgcagtcc tggcaggaag gtcagtgcac cagatattct gaaacctctc aatcaagagg 300
atcccaaatg ctctactaac cctattttga agcaacagaa tctcccatcc agtccggcac 360
ccagtaccat attctctgga ggttttagac acggaagttt aattagcatt gacagcacct 420
gtacagagat gggcaatttt gacaatgcta atgtcactgg agaaatagaa tttgccattc 480
attattgctt caaaacccat tctttagaaa tatgcatcaa ggcctgtaag aaccttgcct 540
atggagaaga aaagaagaaa aagtgcaatc cgtatgtgaa gacctacctg ttgcccgaca 600
gatcctccca gggaaagcgc aagactggag tccaaaggaa caccgtggac ccgacctttc 660
aggagacctt gaagtatcag gtggcccctg cccagctggt gacccggcag ctgcaggtct 720
cggtgtggca tctgggcacg ctggcccgga gagtgtttct tggagaagtg atcattcctc 780

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tggccacgtg ggactttgaa gacagcacaa cacagtcctt ccgctggcat ccgctccggg 840
ccaaggcgga gaaatacgaa gacagcgttc ctcagagtaa tggagagctc acagtccggg 900
ctaagctggt tctcccttca cggcccagaa aactccaaga ggctcaagaa gggacagatc 960
agccatcact tcatggtcaa ctttgtttgg tagtgctagg agccaagaat ttacctgtgc 1020
ggccagatgg caccttgaac tcatttgtta agggctgtct cactctgcca gaccaacaaa 1080
aactgagact gaagtcgcca gtcctgagga agcaggcttg cccccagtgg aaacactcat 1140
ttgtcttcag tggcgtaacc ccagctcagc tgaggcagtc gagcttggag ttaactgtct 1200
gggatcaggc cctctttgga atgaacgacc gcttgcttgg aggaaccaga cttggttcaa 1260
agggagacac agctgttggc ggggatgcat gctcacaatc gaagctccag tggcagaaag 1320
tcctttccag ccccaatcta tggacagaca tgactcttgt cctgcactga catgaaggcc 1380
tcaaggttcc aggttgcagc aggcgtgagg cactgtgcgt ctgcagaggg gctacgaacc 1440
aggtgcaggg tcccagctgg agaccccttt gaccttgagc agtctccatc tgcggccctg 1500
tcccatggct taaccgccta ttggtatctg tgtatattta cgttaaacac aattatgtta 1560
cctaagcctc tggtgggtta tctcctcttt gagatgtaga aaatggccag attttaataa 1620
acgttgttac ccatgaaaaa aaaaaaaa                                    1648
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<210> 45
<211> 313
<212> PRT
<213> Homo sapiens

<220>
<223> Delete: this sequence is a duplicate of Sequence 15

<400> 45

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Met Gly Asn Phe Asp Asn Ala Asn Val Thr Gly Glu Ile Glu Phe Ala
  1               5                  10                  15

Ile His Tyr Cys Phe Lys Thr His Ser Leu Glu Ile Cys Ile Lys Ala
             20                  25                  30

Cys Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Lys Cys Asn Pro
         35                  40                  45

Tyr Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg
     50                  55                  60

Lys Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr
 65                  70                  75                  80

Leu Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln
                 85                  90                  95

Val Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly
            100                 105                 110

Glu Val Ile Ile Pro Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr
        115                 120                 125

Gln Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu
    130                 135                 140

Asp Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu
145                 150                 155                 160

Val Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr
                165                 170                 175

Asp Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala
            180                 185                 190

Lys Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys
        195                 200                 205
```

Gly Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro
210 215 220

Val Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe
225 230 235 240

Ser Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr
245 250 255

Val Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly
260 265 270

Thr Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys
275 280 285

Ser Gln Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu
290 295 300

Trp Thr Asp Met Thr Leu Val Leu His
305 310

<210> 46
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 46
tcgtagagca gcaggtccaa g 21

<210> 47
<211> 1945
<212> DNA
<213> Homo sapiens

<400> 47
aatggaaggg cgtgagcgct tggtccatgc agtgaagctc ttccaacctg ggtcaacgaa 60

aacggagaag aaatggccca agaaatagat ctgagtgctc tcaaggagtt agaacgcgag 120

gccattctcc aggtcctgta ccgagaccag gcggttcaaa acacagagga ggagaggaca 180

cggaaactga aaacacacct gcagcatctc cggtggaaag gagcgaagaa cacggactgg 240

gagcacaaag agaagtgctg tgcgcgctgc cagcaggtgc tggggttcct gctgcaccgg 300

ggcgccgtgt gccggggctg cagccaccgc gtgtgtgccc agtgccgagt gttcctgagg 360

gggacccatg cctggaagtg cacggtgtgc ttcgaggaca ggaatgtcaa aataaaaact 420

ggagaatggt tctatgagga acgagccaag aaatttccaa ctggaggcaa acatgagaca 480

gttggagggc agctcttgca atcttatcag aagctgagca aaatttctgt ggttcctcct 540

actccacctc ctgtcagcga gagccagtgc agccgcagtc ctggcaggtt acaggaattt 600

ggtcagttta gaggatttaa taagtccgtg gaaaatttgt ttctgtctct tgctacccac 660

gtgaaaaagc tctccaaatc ccagaatgat atgacttctg agaagcatct tctcgccacg 720

ggccccaggc agtgtgtggg acagacagag agacggagcc agtctgacac tgcggtcaac 780

gtcaccacca ggaaggtcag tgcaccagat attctgaaac ctctcaatca agaggatccc 840

aaatgctcta ctaaccctat tttgaagcaa cagaatctcc catccagtcc ggcacccagt 900

accatattct ctggaggttt tagacacgga agtttaatta gcattgacag cacctgtaca 960

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accttgaagt atcaggtggc ccctgcccag ctggtgaccc ggcagctgca ggtctcggtg 1260

tggcatctgg gcacgctggc ccggagagtg tttcttggag aagtgatcat tcctctggcc 1320

acgtgggact ttgaagacag cacaacacag tccttccgct ggcatccgct ccgggccaag 1380

gcggagaaat acgaagacag cgttcctcag agtaatggag agctcacagt ccgggctaag 1440

ctggttctcc cttcacggcc cagaaaactc caagaggctc aagaagggac agatcagcca 1500

tcacttcatg gtcaactttg tttggtagtg ctaggagcca agaatttacc tgtgcggcca 1560

gatggcacct tgaactcatt tgttaagggc tgtctcactc tgccagacca acaaaaactg 1620

agactgaagt cgccagtcct gaggaagcag gcttgccccc agtggaaaca ctcatttgtc 1680

ttcagtggcg taaccccagc tcagctgagg cagtcgagct tggagttaac tgtctgggat 1740

caggccctct ttggaatgaa cgaccgcttg cttggaggaa ccagacttgg ttcaaaggga 1800

gacacagctg ttggcgggga tgcatgctca caatcgaagc tccagtggca gaaagtcctt 1860

tccagcccca atctatggac agacatgact cttgtcctgc actgacatga aggcctcaag 1920

gttccaggtt gcagcaggcg tgagg 1945

<210> 48
<211> 610
<212> PRT
<213> Homo sapiens

<400> 48

Met Ala Gln Glu Ile Asp Leu Ser Ala Leu Lys Glu Leu Glu Arg Glu
1 5 10 15

Ala Ile Leu Gln Val Leu Tyr Arg Asp Gln Ala Val Gln Asn Thr Glu
20 25 30

Glu Glu Arg Thr Arg Lys Leu Lys Thr His Leu Gln His Leu Arg Trp
35 40 45

Lys Gly Ala Lys Asn Thr Asp Trp Glu His Lys Glu Lys Cys Cys Ala

```
    50                  55                  60

Arg Cys Gln Gln Val Leu Gly Phe Leu Leu His Arg Gly Ala Val Cys
65                  70                  75                  80

Arg Gly Cys Ser His Arg Val Cys Ala Gln Cys Arg Val Phe Leu Arg
                85                  90                  95

Gly Thr His Ala Trp Lys Cys Thr Val Cys Phe Glu Asp Arg Asn Val
            100                 105                 110

Lys Ile Lys Thr Gly Glu Trp Phe Tyr Glu Glu Arg Ala Lys Lys Phe
        115                 120                 125

Pro Thr Gly Gly Lys His Glu Thr Val Gly Gly Gln Leu Leu Gln Ser
    130                 135                 140

Tyr Gln Lys Leu Ser Lys Ile Ser Val Val Pro Pro Thr Pro Pro Pro
145                 150                 155                 160

Val Ser Glu Ser Gln Cys Ser Arg Ser Pro Gly Arg Leu Gln Glu Phe
                165                 170                 175

Gly Gln Phe Arg Gly Phe Asn Lys Ser Val Glu Asn Leu Phe Leu Ser
            180                 185                 190

Leu Ala Thr His Val Lys Lys Leu Ser Lys Ser Gln Asn Asp Met Thr
        195                 200                 205

Ser Glu Lys His Leu Leu Ala Thr Gly Pro Arg Gln Cys Val Gly Gln
    210                 215                 220

Thr Glu Arg Arg Ser Gln Ser Asp Thr Ala Val Asn Val Thr Thr Arg
225                 230                 235                 240

Lys Val Ser Ala Pro Asp Ile Leu Lys Pro Leu Asn Gln Glu Asp Pro
                245                 250                 255

Lys Cys Ser Thr Asn Pro Ile Leu Lys Gln Gln Asn Leu Pro Ser Ser
            260                 265                 270

Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly Phe Arg His Gly Ser Leu
        275                 280                 285

Ile Ser Ile Asp Ser Thr Cys Thr Glu Met Gly Asn Phe Asp Asn Ala
    290                 295                 300

Asn Val Thr Gly Glu Ile Glu Phe Ala Ile His Tyr Cys Phe Lys Thr
```

305 310 315 320

His Ser Leu Glu Ile Cys Ile Lys Ala Cys Lys Asn Leu Ala Tyr Gly
325 330 335

Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr Val Lys Thr Tyr Leu Leu
340 345 350

Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys Thr Gly Val Gln Arg Asn
355 360 365

Thr Val Asp Pro Thr Phe Gln Glu Thr Leu Lys Tyr Gln Val Ala Pro
370 375 380

Ala Gln Leu Val Thr Arg Gln Leu Gln Val Ser Val Trp His Leu Gly
385 390 395 400

Thr Leu Ala Arg Arg Val Phe Leu Gly Glu Val Ile Ile Pro Leu Ala
405 410 415

Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln Ser Phe Arg Trp His Pro
420 425 430

Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp Ser Val Pro Gln Ser Asn
435 440 445

Gly Glu Leu Thr Val Arg Ala Lys Leu Val Leu Pro Ser Arg Pro Arg
450 455 460

Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp Gln Pro Ser Leu His Gly
465 470 475 480

Gln Leu Cys Leu Val Val Leu Gly Ala Lys Asn Leu Pro Val Arg Pro
485 490 495

Asp Gly Thr Leu Asn Ser Phe Val Lys Gly Cys Leu Thr Leu Pro Asp
500 505 510

Gln Gln Lys Leu Arg Leu Lys Ser Pro Val Leu Arg Lys Gln Ala Cys
515 520 525

Pro Gln Trp Lys His Ser Phe Val Phe Ser Gly Val Thr Pro Ala Gln
530 535 540

Leu Arg Gln Ser Ser Leu Glu Leu Thr Val Trp Asp Gln Ala Leu Phe
545 550 555 560

Gly Met Asn Asp Arg Leu Leu Gly Gly Thr Arg Leu Gly Ser Lys Gly

565 570 575

Asp Thr Ala Val Gly Gly Asp Ala Cys Ser Gln Ser Lys Leu Gln Trp
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Gln Lys Val Leu Ser Ser Pro Asn Leu Trp Thr Asp Met Thr Leu Val
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Leu His
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Ala Ile Leu Gln Val Leu Tyr Arg Asp Gln Ala Val Gln Asn Thr Glu
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Glu Glu Arg Thr Arg Lys Leu Lys Thr His Leu Gln His Leu Arg Trp
35 40 45

Lys Gly Ala Lys Asn Thr Asp Trp Glu His Lys Glu Lys Cys Cys Ala
50 55 60

Arg Cys Gln Gln Val Leu Gly Phe Leu Leu His Arg Gly Ala Val Cys
65 70 75 80

Arg Gly Cys Ser His Arg Val Cys Ala Gln Cys Arg Val Phe Leu Arg
85 90 95

Gly Thr His Ala Trp Lys Cys Thr Val Cys Phe Glu Asp Arg Asn Val
100 105 110

Lys Ile Lys Thr Gly Glu Trp Phe Tyr Glu Glu Arg Ala Lys Lys Phe
115 120 125

Pro Thr Gly Gly Lys His Glu Thr Val Gly Gly Gln Leu Leu Gln Ser
130 135 140

Tyr Gln Lys Leu Ser Lys Ile Ser Val Val Pro Pro Thr Pro Pro Pro
145 150 155 160

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Val Ser Glu Ser Gln Cys Ser Arg Ser Pro Gly Arg Lys Val Ser Ala
                165                 170                 175

Pro Asp Ile Leu Lys Pro Leu Asn Gln Glu Asp Pro Lys Cys Ser Thr
            180                 185                 190

Asn Pro Ile Leu Lys Gln Gln Asn Leu Pro Ser Ser Pro Ala Pro Ser
        195                 200                 205

Thr Ile Phe Ser Gly Gly Phe Arg His Gly Ser Leu Ile Ser Ile Asp
    210                 215                 220

Ser Thr Cys Thr Glu Met Gly Asn Phe Asp Asn Ala Asn Val Thr Gly
225                 230                 235                 240

Glu Ile Glu Phe Ala Ile His Tyr Cys Phe Lys Thr His Ser Leu Glu
                245                 250                 255

Ile Cys Ile Lys Ala Cys Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys
            260                 265                 270

Lys Lys Cys Asn Pro Tyr Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser
        275                 280                 285

Ser Gln Gly Lys Arg Lys Thr Gly Val Gln Arg Asn Thr Val Asp Pro
    290                 295                 300

Thr Phe Gln Glu Thr Leu Lys Tyr Gln Val Ala Pro Ala Gln Leu Val
305                 310                 315                 320

Thr Arg Gln Leu Gln Val Ser Val Trp His Leu Gly Thr Leu Ala Arg
                325                 330                 335

Arg Val Phe Leu Gly Glu Val Ile Ile Pro Leu Ala Thr Trp Asp Phe
            340                 345                 350

Glu Asp Ser Thr Thr Gln Ser Phe Arg Trp His Pro Leu Arg Ala Lys
        355                 360                 365

Ala Glu Lys Tyr Glu Asp Ser Val Pro Gln Ser Asn Gly Glu Leu Thr
    370                 375                 380

Val Arg Ala Lys Leu Val Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu
385                 390                 395                 400

Ala Gln Glu Gly Thr Asp Gln Pro Ser Leu His Gly Gln Leu Cys Leu
                405                 410                 415
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Val Val Leu Gly Ala Lys Asn Leu Pro Val Arg Pro Asp Gly Thr Leu
            420                 425                 430

Asn Ser Phe Val Lys Gly Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu
        435                 440                 445

Arg Leu Lys Ser Pro Val Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys
    450                 455                 460

His Ser Phe Val Phe Ser Gly Val Thr Pro Ala Gln Leu Arg Gln Ser
465                 470                 475                 480

Ser Leu Glu Leu Thr Val Trp Asp Gln Ala Leu Phe Gly Met Asn Asp
                485                 490                 495

Arg Leu Leu Gly Gly Thr Arg Leu Gly Ser Lys Gly Asp Thr Ala Val
            500                 505                 510

Gly Gly Asp Ala Cys Ser Gln Ser Lys Leu Gln Trp Gln Lys Val Leu
        515                 520                 525

Ser Ser Pro Asn Leu Trp Thr Asp Met Thr Leu Val Leu His
    530                 535                 540
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